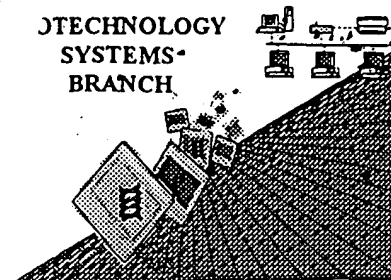


00 11
09 20

TECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/766 511A

Source: O I P E

Date Processed by STIC: 09/19/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

BEST AVAILABLE COPY

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/766 511A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPIA" HEADERS, WHICH WERE INSERTED BY PTO SOFT

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING

DATE: 09/19/2001

PATENT APPLICATION: US/09/766,511A

TIME: 10:55:29.

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Output Set: N:\CRF3\09192001\I766511A.raw

Does Not Comply
Corrected Diskette Needed

Errored: See Page 5 of 83

3 <110> APPLICANT: MCCARTHY, Sean A
 4 FRASER, Christopher C
 5 SHARP, John D
 6 BARNES, Thomas S
 7 KIRST, Susan J
 8 MYERS, Paul S
 9 WRIGHTON, Nicholas
 10 GOODEARL, Andrew
 11 HOLTZMAN, Douglas A
 12 KHODADOUST, Mehran M
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 15 DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER USES
 17 <130> FILE REFERENCE: 210147.0065/65US
 19 <140> CURRENT APPLICATION NUMBER: 09/766,511A
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DATE: 09/19/2001

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TIME: 10:55:29

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RAW SEQUENCE LISTING

DATE: 09/19/2001

PATENT APPLICATION: US/09/766,511A

TIME: 10:55:29

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138 50 55 60

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144 85 90 95

146 Asn Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln

147 100 105 110

149 Gln Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn

150 115 120 125

152 Pro Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser

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RAW SEQUENCE LISTING

DATE: 09/19/2001

PATENT APPLICATION: US/09/766,511A

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/766,511A

DATE: 09/19/2001
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Unknowns must be enumerated in fields
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Notation is incorrect. Should be specific locations
 or a range ~~of~~ over the entire sequence as
 (1...821) or ()... () MH

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 ctggcacccc catgaacca atcttcaga agagcgggtg gtttcaatag tttactggaa 720
 tccttcgaaa tggggtctgg aatgatgtt tctgtgatag taaacacaat tcaatatgtg 780
 aatgaanaa gattacctat gaatgcctgt tattcttaat a 821

VERIFICATION SUMMARY

DATE: 09/19/2001

PATENT APPLICATION: US/09/766,511A

TIME: 10:55:30

Input Set : A:\10147_61.app

Output Set: N:\CRF3\09192001\I766511A.raw

L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:267 M:283 W: Missing Blank Line separator, <400> field identifier
L:268 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9) SEQUENCE:
L:272 M:283 W: Missing Blank Line separator, <400> field identifier
L:273 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:
L:391 M:283 W: Missing Blank Line separator, <400> field identifier
L:392 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (14) SEQUENCE:
L:433 M:283 W: Missing Blank Line separator, <400> field identifier
L:434 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (16) SEQUENCE:
L:438 M:283 W: Missing Blank Line separator, <400> field identifier
L:439 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (17) SEQUENCE:
L:443 M:283 W: Missing Blank Line separator, <400> field identifier
L:444 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:
L:448 M:283 W: Missing Blank Line separator, <400> field identifier
L:449 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:
L:453 M:283 W: Missing Blank Line separator, <400> field identifier
L:454 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (20) SEQUENCE:
L:1749 M:283 W: Missing Blank Line separator, <400> field identifier
L:1750 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (39) SEQUENCE:
L:1754 M:283 W: Missing Blank Line separator, <400> field identifier
L:1755 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (40) SEQUENCE:
L:1896 M:283 W: Missing Blank Line separator, <400> field identifier
L:1897 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (44) SEQUENCE:
L:1901 M:283 W: Missing Blank Line separator, <400> field identifier
L:1902 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (45) SEQUENCE:
L:1906 M:283 W: Missing Blank Line separator, <400> field identifier
L:1907 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (46) SEQUENCE:
L:1911 M:283 W: Missing Blank Line separator, <400> field identifier
L:1912 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (47) SEQUENCE:
L:1916 M:283 W: Missing Blank Line separator, <400> field identifier
L:1917 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (48) SEQUENCE:
L:1921 M:283 W: Missing Blank Line separator, <400> field identifier
L:1922 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (49) SEQUENCE:
L:1926 M:283 W: Missing Blank Line separator, <400> field identifier
L:1927 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (50) SEQUENCE:
L:2118 M:283 W: Missing Blank Line separator, <400> field identifier
L:2119 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (56) SEQUENCE:
L:2123 M:283 W: Missing Blank Line separator, <400> field identifier
L:2124 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (57) SEQUENCE:
L:2128 M:283 W: Missing Blank Line separator, <400> field identifier
L:2129 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (58) SEQUENCE:
L:2133 M:283 W: Missing Blank Line separator, <400> field identifier
L:2134 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (59) SEQUENCE:
L:2209 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:61
L:2209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:2326 M:283 W: Missing Blank Line separator, <400> field identifier
L:2327 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (66) SEQUENCE:
L:2331 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY

DATE: 09/19/2001

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Input Set : A:\10147_61.app

Output Set: N:\CRF3\09192001\I766511A.raw

L:2332 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (67) SEQUENCE:
L:2336 M:283 W: Missing Blank Line separator, <400> field identifier
L:2337 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (68) SEQUENCE:
L:2341 M:283 W: Missing Blank Line separator, <400> field identifier
L:2342 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (69) SEQUENCE:
L:2346 M:283 W: Missing Blank Line separator, <400> field identifier
L:2347 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (70) SEQUENCE:
L:2517 M:283 W: Missing Blank Line separator, <400> field identifier
L:2518 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (74) SEQUENCE:
L:2522 M:283 W: Missing Blank Line separator, <400> field identifier
L:2523 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (75) SEQUENCE:
L:2527 M:283 W: Missing Blank Line separator, <400> field identifier
L:2528 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (76) SEQUENCE:
L:2532 M:283 W: Missing Blank Line separator, <400> field identifier
L:2533 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (77) SEQUENCE:
L:2537 M:283 W: Missing Blank Line separator, <400> field identifier
L:2538 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (78) SEQUENCE:
L:2542 M:283 W: Missing Blank Line separator, <400> field identifier
L:2543 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (79) SEQUENCE:
L:2547 M:283 W: Missing Blank Line separator, <400> field identifier
L:2548 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (80) SEQUENCE: